

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 4, 2002, 01:26:26 ; Search time 15.194 Seconds

(without alignments)  
1105.559 Million cell updates/sec

Title: US-09-805-550-2

Perfect score: 2036  
Sequence: 1 MLNWKTKTNGTNEIEASPD.....EEETANYLLDHGHEPDDQOO 405

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	632	31.0	409 1	R23B_HUMAN
2	623.5	30.6	416 1	R23B_MOUSE
3	588	28.9	368 1	RH23_SCHPO
4	577	28.3	363 1	R23A_MOUSE
5	573	28.1	363 1	R23A_HUMAN
6	483.5	23.7	398 1	R23B_YEAST
7	167	8.2	373 1	DSK2_YEAST
8	154.5	7.6	354 1	YANG_SCHPO
9	149	7.3	1083 1	T2D3_HUMAN
10	144	7.1	637 1	ODP2_AZOVI
11	140.5	6.9	1509 1	GSRL_HUMAN
12	140	6.9	2441 1	CBP_MOUSE
13	139.5	6.9	1132 1	BAT3_HUMAN
14	137.5	6.8	547 1	ODP2_PSEAE
15	137.5	6.8	552 1	EPG1_CANAL
16	137.5	6.8	865 1	CPN_DROME
17	136	6.7	743 1	OCY1_HUMAN
18	136	6.7	797 1	PART_YEAST
19	135	6.6	352 1	ALGP_PSEAE
20	135	6.6	1048 1	SR4A_RAT
21	134.5	6.6	699 1	VGLG_HSV2H
22	133.5	6.6	1157 1	SR4A_HUMAN
23	133.5	6.6	2442 1	CBP_HUMAN
24	131	6.4	1783 1	RAA3_CHIRE
25	130	6.4	392 1	HME1_HUMAN
26	129.5	6.4	1772 1	MSPI_PLAYO
27	129	6.3	511 1	P60_LISGR
28	129	6.3	688 1	DP3X_HAEIN
29	129	6.3	1794 1	YAVI_SCHPO
30	127.5	6.3	815 1	RBMS_HUMAN
31	127	6.2	497 1	HMS_DROME
32	127	6.2	1544 1	TUSP_HUMAN
33	126.5	6.2	721 1	YK82_MYCTU

34	126.5	6.2	825 1	ICP0_HSV2H	P28284 herpes simp
35	126.5	6.2	1115 1	NCAL_MOUSE	P13595 mus musculu
36	125.5	6.2	1211 1	BUN2_DROME	024523 drosophila
37	125.5	6.2	2090 1	N214_HUMAN	P35658 homo sapien
38	125	6.1	2459 1	MABP_RAT	P15205 ratu
39	124.5	6.1	3149 1	TEGU_EBV	P03186 epstein-bar
40	124	6.1	2414 1	P300_HUMAN	009472 homo sapien
41	123.5	6.1	1596 1	MAM_DROME	P21519 drosophila
42	123	6.0	339 1	MP5B_LOLPR	040237 lolium pere
43	123	6.0	483 1	PREG_NEUCR	006712 neosporea
44	123	6.0	901 1	A180_MOUSE	061548 mus musculu
45	123	6.0	1326 1	BCC2_ACEXY	082861 acetobacter

## ALIGNMENTS

RESULT 1  
ID R23B\_HUMAN STANDARD; PRT; 409 AA.  
AC P54727;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 15-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE UV excision repair protein RAD23 homolog B (HHR23B) (XP-C repair  
DE complementing complex 58 kDa protein) (P58).  
GN RAD23B.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=94222030; PubMed=8168482;  
RA Mesutani K., Sugawara K., Yanagisawa J., Sonoyama T., Ue M.,  
RA Enomoto T., Takio K., Tanaka K., van der Spek P.J., Bootsma D.,  
RA Hoeijmakers J.H.J., Hanaoka F.;  
RT "Purification and cloning of a nucleotide excision repair complex  
RT involving the xeroderma pigmentosum group C protein and a human  
RT homologue of yeast RAD23.";  
RT EMBO J. 13:1831-1843(1994).  
CC -!- FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA  
CC DAMAGE RECOGNITION AND/OR IN ALTERING CHROMATIN STRUCTURE TO  
CC ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES.  
CC -!- SUBUNIT: Heterodimer of a 125 kDa subunit (p125) and of a  
CC 58 kDa subunit (p58). Interacts with MTD.  
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).  
CC -!- DOMAIN: The ubiquitin-like domain mediates interaction with MTD.  
CC -!- SIMILARITY: CONTAINS 2 UBA DOMAINS.  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL: D21090; BAA04652.1; -.  
CC HSSP: P54725; IDV0.  
CC Genew: HGNC:9813; RAD23B.  
CC KIM: 6000062; -.  
CC InterPro: IPR004806; Rad23.  
CC InterPro: IPR000449; UBA\_domain.  
CC InterPro: IPR000626; Ubiquitin.  
CC Pfam: PF00240; Ubiquitin\_1.  
CC Pfam: PF00627; UBA\_2.  
CC SMART: SM00165; UBA; 2.  
CC SMART: SM00213; UBO; 1.  
CC TRIGRAMS: TRIGR00601; rad23; 1.  
CC PROSITE: PS50053; UBOUTITIN\_2; 1.  
CC DNA damage; DNA repair; Nuclear protein.  
KW

FT DOMAIN 1 79 UBIQUITIN-LIKE.  
 FT DOMAIN 103 106 POLY-THR.  
 FT DOMAIN 254 260 POLY-ALA.  
 FT DOMAIN 261 269 POLY-THR.  
 FT DOMAIN 336 348 POLY-GLY.  
 SQ SEQUENCE 409 AA: 43171 MW: C026C78273BCB289 CRC64:

Query Match 31.0%; Score 632; DB 1; Length 409;  
 Best Local Similarity 34.1%; Pred. No. 1,1e-28;  
 Matches 150; Conservative 82; Mismatches 138; Indels 70; Gaps 11;

1 MKLNVKTLKGTNEIEASPDASVADYKRIETTGOSTYRADQOMLIYQKILKDETTLE 60  
 1 MOVTLTKTLOOQTFKIDIDEETVKAKKEISEKKGDAFPVAGOKLIYAGKILINDTALK 60  
 61 SNGVAENSLVYMLSKAKASSGASTATTAKAPA-----TLQAPAAVAPAAV 109  
 61 EYKIDKKNVYVMTKPKAVSTPAATQOASAPSTTAVTSSTTTVAQAPFV-PALAP 119  
 110 ARTPTQ-----APVATAEPAAPSVQQAAPAT-VAATD-----ADYISQ 149  
 120 TSTPASITPASATASSEPAPASAKQEKPAEKPAETPVATSPATDSTGSSRSMLFED 179  
 150 AASNLVEGNLEQTLQIILDMGGTWERDVTYVRLRAAYNNPRAIDYLSGIPENVAO 209  
 180 ATSAVTGSGYENMTVEISMKG---YREQVIALALRASFNNDRAVEYILMGIPGDRSO 236  
 210 PVARAPAGQOTNOQASPAOPAVALPVOPSPASAGPNANPLNFPQGVPSGSGSNPVVP 269  
 237 AVADPPQA-----STGAPQSSAVAAAAATTAT-----TTSSGHP----- 275  
 270 GAGSGALDLRLQPOFALLQVQANPOLPMLQELQKONQIILQENQAEFLRLYN 329  
 276 -----LEFLRNQOPQOQORQIILQONPSLLPALQOIGRENPOLLOISQHEHFIOLN 329  
 330 E-----SPGCGPGNLTGOLAAAVP---OTLVTPEERAIORLEGMGFRELVEFVA 381  
 330 EYQVQEGGSGGGGGGGGIAEGSGHMYIQTVEKRIERLKLGFPEGLVIOAYTA 389  
 382 CNKDELTANYLLDHGHEFD 401  
 390 CEKNEMIANFLQONFDED 409

RESULT 2  
 R3B\_MOUSE STANDARD: PRT; 416 AA.  
 ID R23B\_MOUSE  
 AC P54728;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE UV excision repair protein RAD23 homolog B (MHR23B) (XP-C repair  
 DE complementing complex 58 kDa protein) (P58).  
 GN RAD23B OR MHR23B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OK NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/c; TISSUE-Testis;  
 RX MEDLINE=96403997; PubMed=8808275;  
 RA van der Spek P.J., Visser C.E., Hanacka F., Smit B.,  
 RA Hagemeijer A., Bootsma D., Hoeljmakers J.H.J.;  
 RT "Cloning, comparative mapping, and RNA expression of the mouse  
 RT homologues of the Saccharomyces cerevisiae nucleotide excision repair  
 RT gene RAD23."  
 RL Genomics 31:20-27(1996).  
 CC -1- FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA  
 CC DAMAGE RECOGNITION AND/OR IN ALTERING CHROMATIN STRUCTURE TO  
 CC ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES.  
 CC -1- SUBUNIT: HETERODIMER OF A 125 kDa SUBUNIT (P125) AND OF A  
 CC 58 kDa SUBUNIT (P58).

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 UBA DOMAINS.  
 CC -----  
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 CC -----

DR EMBL: X92411; CA63146.1; -  
 DR HSSP: P54725; IDV0.  
 DR MGD: MGI:105128; Rad23b.  
 DR InterPro: IPR004806; Rad23.  
 DR InterPro: IPR004449; UBA.domain.  
 DR InterPro: IPR00626; Ubiquitin.  
 DR Pfam: PF00240; Ubiquitin; 1.  
 DR Pfam: PF00627; UBA; 2.  
 DR SMART: SM00165; UBA; 2.  
 DR SMART: SM00213; UBO; 1.  
 DR TIGRFAMS: TIGR00601; rad23; 1.  
 DR PROSITE: PS50053; UBIQUITIN\_2; 1.  
 DR DNA damage; DNA repair; Nuclear protein.  
 KW DOMAIN 1 79 UBIQUITIN-LIKE.  
 FT DOMAIN 255 261 POLY-ALA.  
 FT DOMAIN 262 270 POLY-THR.  
 FT DOMAIN 336 355 POLY-GLY.  
 SQ SEQUENCE 416 AA: 43516 MW: 13E0245AD892205 CRC64:

Query Match 30.6%; Score 623.5; DB 1; Length 416;  
 Best Local Similarity 32.4%; Pred. No. 3.3e-28;  
 Matches 146; Conservative 85; Mismatches 136; Indels 83; Gaps 10;

1 MKLNVKTLKGTNEIEASPDASVADYKRIETTGOSTYRADQOMLIYQKILKDETTLE 60  
 1 MOVTLTKTLOOQTFKIDIDEETVKAKKEISEKKGDAFPVAGOKLIYAGKILSDTALK 60  
 61 SNGVAENSLVYMLSKAKA-----SSGASTATTAKAPATLQAPAAVAPAAV 110  
 61 EYKIDKKNVYVMTKPKAVTAVPATPQSSPTPTVSSPAY-----AAQAPAPTPA 116  
 111 RTPTQAPVAT-----AETAP-----PSVOPQAPAPATVATAD-----ADV 146  
 117 LAPSTPASTTPASTTASSEPAPACATQEPKPAEKPAOTPVLTSPAPADSPRGSSRNL 176  
 147 YQASNLVEGNLEQTLQIILDMGGTWERDVTYVRLRAAYNNPRAIDYLSGIPENY 206  
 177 FEDATSAVTGSGYENMTVEISMKG---YREQVIALALRASFNNDRAVEYILMGIPDR 233  
 207 EAPVAPARAPAAQOTNOQASPAOPAVALPVOPSPASAGPNANPLNFPQGVPSGSGSNP 266  
 234 ESQAVNDPPQAVST-----GTQSPAVAAAAATTAT-----TTSSGHP- 275  
 267 VVPGAGSALDLRLQPOFALLQVQANPOLPMLQELQKONQIILQENQAEFLR 326  
 276 -----LEFLRNQOPQOQORQIILQONPSLLPALQOIGRENPOLLOISQHEHFIQ 326  
 327 LVNESP-----GPGGNLTGOLAAAVPOTLVTPEERAIORLEGMGFN 371  
 327 MLNEPVQEGGSGGGGGGGGIAEGSGHMYIQTVEKRIERLKLALGFP 386  
 372 RELVEFPACNKNDELTANYLLDHGHEFD 401  
 387 EGLVIOATFACEKNEMIANFLQONFDED 416

RESULT 3  
 RH23\_SCHPO STANDARD: PRT; 368 AA.  
 ID RH23\_SCHPO  
 AC 074803;  
 DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE UV excision repair protein rhp23 (RAD23 homolog).  
 GN RHP23 OR SPBC2D10.12.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetales;  
 OC Schizosaccharomycetes.  
 ON NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.  
 RC STRAIN=SP223;  
 RX PubMed=11786722;  
 RA Elder R.T., Song X.-Q., Chen M., Hopkins K.M., Lieberman H.B.,  
 RA Zhao Y.;  
 RT "Involvement of rhp23, a Schizosaccharomyces pombe homolog of the  
 RT human HHR23A and Saccharomyces cerevisiae Rad23 nucleotide excision  
 RT repair genes, in cell cycle control and protein ubiquitination.";  
 RL Nucleic Acids Res. 30:581-591(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tiley A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Gysmonprez B.,  
 RA Welfens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Babel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Medler H., Wambut R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,  
 RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Kocher M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potaschkin J.,  
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 RN [3]  
 RP CHARACTERIZATION.  
 RX PubMed=10652237;  
 RA Lombers M., Goeloe J.I., den Dulk H., Brandsma J.A., Brower J.;  
 RT "Identification and characterization of the rhp23(+) DNA repair gene  
 RT in Schizosaccharomyces pombe.";  
 RL Blochm. Biophys. Res. Commun. 268:210-215(2000).  
 CC -1- FUNCTION: Involved in postreplication repair of UV-damaged DNA.  
 CC Postreplication repair functions in gap-filling of a daughter  
 CC strand on replication of damaged DNA.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: AF174293; AAD51975.1; -;  
 CC DR EMBL: AL031788; CAA21170.1; -;  
 CC DR HSSP: P34725; IDV0.

DR InterPro: IPR000449; UBA.  
 DR InterPro: IPR000626; Ubiquitin.  
 DR Pfam: PF00627; UBA; 2.  
 DR Pfam: PF00240; ubiquitin; 1.  
 DR SMART: SM00165; UBA; 2.  
 DR SMART: SM00213; UBA; 1.  
 DR PROSITE: PS50053; UBIQUITIN\_2; 1.  
 DR DNA damage; DNA repair; Nuclear protein.  
 FT DOMAIN 1 77 UBIQUITIN-LIKE.  
 FT DOMAIN 119 122 POLY-ALA.  
 FT DOMAIN 205 208 POLY-GLN.  
 SQ SEQUENCE 368 AA; 5CE75EB7E190EFD4 CRC64;  
 Query Match 28.9%; Score 588; DB 1; Length 368;  
 Best Local Similarity 35.3%; Pred. No. 2.8e-26;  
 Matches 146; Conservative 72; Mismatches 138; Indels 58; Gaps 13;  
 QY 1 MKNVKTLLKGTNEET-EASPDASVADYKRIILETTOGOSTYRADQOMLTIGYKLIKDETL 59  
 DB 1 MNLTFKNLQOQKEVYISDVSAADTKISELKERIQT---QONTEVEROKLIYSGRIADDKTV 57  
 QY 60 ESNQVANSFLVIMLSKAKSSGSGATATKAPATLAOPAPAPAPAPAPAPAPAPAPAPAP 119  
 DB 58 GEYIKQEDIVICVNSPKTSTS-----TPKSASFPAP-NPPASVPEKKVEAPSS 106  
 QY 120 TAETAPSPVOPOAPAPAT---VAATDADYYSQASMLVGNMIEQTIQOILDMGGGTWE 176  
 DB 107 TVASTSTTQTVAAASNDPTATSEAP---DANLAVAGAKNVAENVMENG---YE 160  
 QY 177 RDTYVRLRAAYNPERAIDYLSGIRENV---EAQVAPAPAPAGQOTNOAASPAPAV 233  
 DB 161 RSEVERMRAPAFNPNDAVEVILLGIPEDILNRQRESAALAAQOQOSALA----- 213  
 QY 234 ALPQSPASAGPAPANPLNFPQGVPSGSGNPVPE-AGSGALDALRQLPQALQIV 292  
 DB 214 -----PTSTG---QPANLFEQALSENENQEPSTVGDDPLGTRISIPQQLQIV 263  
 QY 293 QANPQILQPMLOELGKONPQILRLIOENQAEFLRVNESEGG---PGCNILQOLAAPV 349  
 DB 264 QONQOMLETILQIQGGQDPALQAQITQNPFAFIQDLMEAGEGESALPSGGI----- 314  
 QY 350 QTLVTPEERPAIORLEMGFNRELYLVFPACKDELTANLYLDHGHEFDDQ 403  
 DB 315 -QIDITQEESESIDRLCOLGPRNIVIOAVLADCKNEELNAYLFEHGHESE 367  
 RESULT 4  
 R23A\_MOUSE  
 ID R23A\_MOUSE STANDARD; PRT; 363 AA.  
 AC P54726;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE UV excision repair protein Rad23 homolog A (HHR23A).  
 GN RAD23A OR MHR23A.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Testis;  
 RX MEDLINE=96403997; PubMed=808275;  
 RA van der Spek P.J., Visser C.E., Hanaoka F., Smit B.,  
 RA Hagemeljer A., Bootsma D., Hoeijmakers J.H.J.;  
 RT "Cloning, comparative mapping, and RNA expression of the mouse  
 RT homologues of the Saccharomyces cerevisiae nucleotide excision repair  
 RT gene RAD23.";  
 RL Genomics 31:20-27(1996).  
 CC -1- FUNCTION: Involved in postreplication repair of UV-damaged DNA.  
 CC Postreplication repair functions in gap-filling of a daughter  
 CC strand on replication of damaged DNA (potential).  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.  
CC -1- SIMILARITY: CONTAINS 2 UBA DOMAINS.  
CC -----  
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CC -----  
DR EMBL: X92410; CAA63145.1; -  
DR HSSP: P54725; IDV0.  
DR MGD: MGI:105126; Rad23a.  
DR InterPro: IPR004806; Rad23.  
DR InterPro: IPR000449; UBA\_domain.  
DR InterPro: IPR000626; Ubiquitin.  
DR Pfam: PF00240; ubiquitin; 1.  
DR Pfam: PF00627; UBA; 2.  
DR SMART: SM00165; UBA; 2.  
DR SMART: SM00213; UBO; 1.  
DR TIGRfams: TIGR00601; rad23; 1.  
DR PROSITE: PS50053; UBIQUITIN\_2; 1.  
DR DNA damage: DNA repair: Nuclear protein.  
KM DOMAIN 1 79 UBIQUITIN-LIKE  
FT SEQUENCE 363 AA; 39769 MW; 67EAB96EBEAS203 CRC64;  
SQ  
Query Match 28.3%; Score 577; DB 1; Length 363;  
Best Local Similarity 33.4%; Pred. No. 1.9e-25;  
Matches 140; Conservative 77; Mismatches 124; Indels 78; Gaps 13;  
QY 3 LNVKTLKGTFEIASPDASVADVKRIETTGQSTYRADQOQLYOGKILKDETTLESN 62  
DB 5 IRLKTLQOQTFKIRMBDETVAVLKEKIEAKGRAPVAGOKILYAGKILSDVPIDRY 64  
QY 63 GVAENSLVYIMSKAKASSGASTATTAAPATLAQPAAPVAP--AAVAPRP----- 113  
DB 65 HIDEKFEVYVMTAKA--GOGISAPPEA--SPTAVPEPSTPEPPVILASGSHPPYRSREK 122  
QY 114 TQAPVATAPSPVQQAAPATVATDADVYSGAASNLVFGNNLEQTIOOILDMGCG 173  
DB 123 SPSESTTTSPESISGVSPPSSGSGRED-----AASLTVTSGEYETMLTEIMSG-- 174  
QY 174 THERDVTVAALAAVNNPRAIDLYLSGTPENVEAPVAPARAQO--QTNOQAASPAQDA 232  
DB 175 -TEREVVAVALASVNNPRAVEYLLTGIGSPE-----PEKSGVDSORAREOPATEA 226  
QY 223 VALPVQPSASAGPNANPLNLFPGVPSGSGNPGVPGAGSGALDRLRLOPQALLOLV 292  
DB 227 -----AGENPLELRLQPOFOFNKROYI 248  
QY 293 QANPOLQPMQLGKONPOLRLIQENQAEFLRLVNESPEGCGNT-----LQQLAA 346  
DB 249 QONPALPALLOQLGQENPOLLOQISRHQEQFIQMLNEPP--GELADISDVEGEVGAIGE 306  
QY 347 AVPQOT--LVTPEPERAIOIRLEGMGFNRLVLEVPFACKDEELTANYLLDGHEDDQ 403  
DB 307 EAPQNYIOTVYQEKAEIRLKAIGPESLVIOAYFACEKNEMLANFL--SQNFDE 363  
RESULT 5  
R23A\_HUMAN  
ID R23A\_HUMAN STANDARD; PRT; 363 AA.  
AC P54725;  
DT 01-OCT-1996 (Rel. 34; Created)  
DT 01-OCT-1996 (Rel. 34; Last sequence update)  
DT 15-JUN-2002 (Rel. 41; Last annotation update)  
DE UV excision repair protein RAD23 homolog A (HHR23A).  
GN RAD23A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-9422030; PubMed-8168482;  
RA Masutani C., Sugawara K., Yanagisawa J., Sonoyama T., Ui M.,  
RA Enomoto T., Takio K., Tanaka K., van der Spek P.J., Bootsma D.,  
RA Hoeijmakers J.H.J., Hanoka F.,  
RT "Purification and cloning of a nucleotide excision repair complex  
RT involving the xeroderma pigmentosum group C protein and a human  
RT homologue of yeast RAD23.";  
RL EMBO J. 13:1831-1843(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Lamerdin J., McCreedy P., Stijlwaagen S., Ramirez M., Carrano A.;  
RN Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP STRUCTURE BY NMR OF 319-363.  
RX MEDLINE-99061330; PubMed-9846873;  
RA Dieckmann T., Withers-Ward E.S., Jarosinski M.A., Liu C.F.,  
RA Chen I.S.Y., Feilgen J.,  
RT "Structure of a human DNA repair protein UBA domain that interacts  
RT with HIV-1 Vpr.";  
RL Nat. Struct. Biol. 5:1042-1047(1998).  
RN [4]  
RP STRUCTURE BY NMR OF 319-363.  
RX MEDLINE-20541363; PubMed-11087358;  
RA Withers-Ward E.S., Mueller T.D., Chen I.S.Y., Feilgen J.,  
RT "Biochemical and structural analysis of the interaction between the  
RT UBA(2) domain of the DNA repair protein HHR23A and HIV-1 Vpr.";  
RL Biochemistry 39:14103-14112(2000).  
CC -1- FUNCTION: Involved in postreplication repair of UV-damaged DNA.  
CC Postreplication repair functions in gap-filling of a daughter  
CC strand on replication of damaged DNA (Potential).  
CC -1- SUBUNIT: Interacts with MJD.  
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
CC -1- DOMAIN: The ubiquitin-like domain mediates interaction with MJD.  
CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.  
CC -1- SIMILARITY: CONTAINS 2 UBA DOMAINS.  
CC -----  
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CC -----  
DR EMBL: D21235; BAA04767.1; -  
DR EMBL: AD000092; AAB51177.1; -  
DR PDB: IDV0; 11-FEB-00.  
DR GENE: HGNC:9612; RAD23A.  
DR MIM: 600061; -  
DR InterPro: IPR004806; Rad23.  
DR InterPro: IPR000449; UBA\_domain.  
DR InterPro: IPR000626; Ubiquitin.  
DR Pfam: PF00240; ubiquitin; 1.  
DR Pfam: PF00627; UBA; 2.  
DR SMART: SM00165; UBA; 2.  
DR SMART: SM00213; UBO; 1.  
DR TIGRfams: TIGR00601; rad23; 1.  
DR PROSITE: PS50053; UBIQUITIN\_2; 1.  
DR DNA damage: DNA repair: Nuclear protein: 3D-structure.  
KM DOMAIN 1 81 UBIQUITIN-LIKE  
FT SEQUENCE 363 AA; 39609 MW; C4E47E9313B84785 CRC64;  
SQ  
Query Match 28.1%; Score 573; DB 1; Length 363;  
Best Local Similarity 33.3%; Pred. No. 1.9e-25;  
Matches 139; Conservative 79; Mismatches 124; Indels 76; Gaps 13;  
QY 3 LNVKTLKGTFEIASPDASVADVKRIETTGQSTYRADQOQLYOGKILKDETTLESN 62  
DB 5 IRLKTLQOQTFKIRMBDETVAVLKEKIEAKGRAPVAGOKILYAGKILSDVPIDRY 64  
QY 63 GVAENSLVYIMSKAKASSGASTATTAAPATLAQPAAPVAP--VPAASVARTPTQAPVA 119

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Db 65 RIDKKNVVMVTKTKA---GGGTSAPPEASPTAPSSSTFPAPYSGMSHP---PAA 118
QY 120 TAETAP-----PSYQOAPAAATVAATDADVYSOAASNLFVGNLQITQIOLDMGGCT 174
Db 119 REDKSPSEASPTTSPESV-SGSVPSSGSSGREDASTLVTSGETYETMLTEISMG--- 174
QY 175 WERTVYRALRAAYNNPERAIDYISGIPENVEAQVAPARAQO-QTNOOASPAQAPAV 233
Db 175 YERERVYAAALRASYNHRAVEYLLTGITPGSP-----PEHGSVOESQVSEDPATEA- 226
QY 234 ALVQVPSAPAGPRANPLNFPGVPSGSGSNPGVPGAGSALDALQOLQOFOALLQVQ 293
Db 227 -----AGENPLEFLKDOQPOFQNMKROYIQ 249
QY 294 ANFOILQPMLOELGKONPQILRLIQENQAEFLRLVNESPEGPGCNI-----LGOATAA 347
Db 250 QNALLPALLQOLQOGEHPQILQISRHQEQFIQMLNEPP--GELADISDVEGEGALGEE 307
QY 348 VPQT--LTVPREERAIQRLGEGNFELVLEVFACNKEDELTANYLLDHGHEFDQ 403
Db 308 APOMNVIQVTPQEKALERKALGFPESLVYQAFACEKNENLAANFL--SQNFDE 363
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RESULT 6
RA23_YEAST
ID RA23_YEAST STANDARD; PRT; 398 AA.
AC P32628;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE UV excision repair protein RAD23.
GN RAD23 OR YEL037C OR SYGP-ORF29.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID:4932;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-94067136; PubMed-8246991;
RA Watkins J.F., Sung P., Prakash S.;
RT "The Saccharomyces cerevisiae DNA repair gene RAD23 encodes a nuclear
RT protein containing a ubiquitin-like domain required for biological
RT function."
RL Mol. Cell. Biol. 13:7757-7765(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp C.,
RA Mei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-S288c / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berrio A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mysenale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Patel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Mei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN-B-6441;
RA MEDLINE-94016558; PubMed-841151;
RA Melnick L., Sherman F.;
RT "The gene clusters ARC and COR on chromosomes 5 and 10, respectively,
RT of Saccharomyces cerevisiae share a common ancestry."
RL J. Mol. Biol. 233:372-388(1993).
CC - SUBCELLULAR LOCATION: Nuclear (Probable).
CC - SIMILARITY: CONTAINS 1 UBIOQUITIN-LIKE DOMAIN.
CC -----
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CC EMBL; L25428; AAA16070.1; -
DR EMBL; U18779; AAB65005.1; -
DR EMBL; L22172; AAA34935.1; -
DR EMBL; L22173; AAA34938.1; -
DR EMBL; S65964; AAD13972.1; -
DR EMBL; S66117; AAB28441.1; -
DR PIR; S30845; S30845.
DR HSP; P54725; IDV0.
DR SGD; S0000763; RAD23.
DR InterPro: IPR004806; Rad23.
DR InterPro: IPR000449; UBA_domain.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam; PF00627; UBA; 2.
DR SMART; SM00165; UBA; 2.
DR SMART; SM00213; UBQ; 1.
DR TIGRfam; TIGR00601; rad23; 1.
DR PROSITE; PS50053; UBIOQUITIN_2; 1.
KW DNA damage; DNA repair; Nuclear protein.
FT DOMAIN 1 77 UBIOQUITIN-LIKE.
FT CONFICT 277 277
SQ SEQUENCE 398 AA; 42366 MW; B3F0436DAB6B833 CRC64;
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Query Match 23.7%; Score 483.5; DB 1; Length 398;  
Best Local Similarity 32.3%; Pred. No. 2e-20;  
Matches 142; Conservative 65; Mismatches 144; Indels 89; Gaps 18;

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QY 1 MKLWKLTKGNFEIRASPDASVADVKRIETGQSGYRADQOM-LIYGKTIKDEFTL 59
Db 2 VSLTFKFKKKKVPDLPSWTILETK---TKLAQISCESEQIKLVSQKVLQDSKTV 57
QY 60 ESNQVAENSLVIMLSRAKASSSGASTATYAKAPATIAQAPAPVAPASVAKRP----- 113
Db 58 SEGGLKODQDYVFNVSQK-----STRTKVTPE-----PLAPES--ATTPGRENST 101
QY 114 -----TOAPVATTAETAPSPVOPQAPATVAATDADVYSOAASNLFVGNLQITQIOL 168
Db 102 EASPTDASAPATAEAGSQPOEQTATERTESA-----STPGFVGTETNETIRIM 156
QY 169 DMGGGTWERDITVVALRAAYNNPERAIDYLSGIPENVEAQVAPARAQOQTNOOASP 228
Db 157 EMG---TQREVERALRAAFNNPDAVEYLLMGIPENL-----RQPPQOQT---AAAA 204
QY 229 AQPVALVPQSPASAGPNAPLMLFPGVPSGSGSNPGVPGAGSALDALROLP----- 283
Db 205 EQPSTAATTAATPAED-----DLFQAAGCAASSAL-GTTCGATDAAGGPPSGTG 256
QY 284 -----QFOALLQVQANFOILQPMLOELGKONPQILRLIQENQAEFLRLVNES----- 331
Db 257 LTVEDELTLRQVVGNGENALPLLENISARYPQIREHMANPEVFVSLTAVAGDNQDV 316
QY 332 PEG-----GGGNILGOLAA-VPO-----LTVPREERAIQRLGEGNFRELAYLE 377
Db 317 MEGADDMYEGEDIEVTGAAAGAGGEGSGSFQVDYTPEDDAISRICEIGFERDLYIQ 376
QY 378 VFACNKNDEELTANYLL-DH 396
Db 377 VFACNKNKEEAANILFSDH 396
RESULT 7
DSK2_YEAST
ID DSK2_YEAST STANDARD; PRT; 373 AA.
AC P48510;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
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16-OCT-2001 (rel. 40, last annotation update)  
 DSK2 OR SH2 OR YMR276W OR YMR021.02.  
 Saccharomyces cerevisiae (Baker's yeast).  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 NCBI\_TaxID=4932;  
 (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C;  
 RX MEDLINE=96281973; PubMed=8682868;  
 RA Biggins S., Ivanovska I., Rose M.D.;  
 RT "Yeast ubiquitin-like genes are involved in duplication of the  
 RT microtubule organizing center.";  
 RT J. Cell Biol. 133:1331-1346(1996).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-S288C;  
 RX Pearson D., Bowman S., Barrell B.G., Rajandream M.A.;  
 RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INVOLVED, WITH RAD23 IN SPINDLE POLE BODY DUPLICATION.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- SIMILARITY: To S. pombe SPAC26A3.16.  
 CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.  
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 CC EMBL: L40587; AAB07267.1;  
 DR EMBL: 249704; CAAB9774.1;  
 DR HSSP: 015843; IND0.  
 DR SGD: S0004889; DSK2.  
 DR InterPro: IPR000449; UBA\_domain.  
 DR InterPro: IPR000526; Ubiquitin.  
 DR Pfam: PF00240; ubiquitin.1.  
 DR Pfam: PF00627; UBA.1.  
 DR SMART: SM00165; UBA.1.  
 DR SMART: SM00213; UBO.1.  
 DR PROSITE: PS00299; UBIQUITIN\_1; 1.  
 DR PROSITE: PS00503; UBIQUITIN\_2; 1.  
 DR Nuclear protein.  
 KW DOMAIN 1 76 UBIQUITIN-LIKE.  
 FT CONFLICT 109 109 R -> A (IN REF. 2).  
 FT CONFLICT 296 296 R -> A (IN REF. 2).  
 FT SEQUENCE 373 AA; 39516 MW; 25DF82B9DB67DF6 CRC64;  
 SQ  
 Query Match 8.2%; Score 167; DB 1; Length 373;  
 Best Local Similarity 23.2%; Pred. No. 0.0081;  
 Matches 94; Conservative 47; Mismatches 168; Indels 96; Gaps 19;  
 1 MLNWKTKLGN-FEIEASPDASVADVKRIETGQSTYRADQMLTYQGLNDELTL 59  
 1 MSINHIKSGDKMEVNVAPSTVLOFKKAIKANG--IPVANOIRLISYKILKDKQIV 57  
 60 EENGAENEFVIMSKAK--ASSSGASTATTAAPATLAPAPVAPAAVAPRPTQA 116  
 58 ESYHIDGHSVILVKSQPPQOTASAGANNATATGA-----AACTGATPNN 104  
 117 PVATAEAPSPVQPAAPAAATDADYVQAASNLVFGNNLQOTIQLIDMGCTWE 176  
 105 S-GGGRGFPLADLTSAKAGLYNMPADMFPGDGL--NDSNNDDELLRM---ME 156  
 177 RDTVYRALFAAYNPERALDIYISGIPENVEAPVAPAPAAQQTNQAAAP---AQA 232  
 157 NFIFOSNNEMLSNPQ-MIDFMIQSNPOLQAMGPQARQMLQSPMFRQMLTNDPIMQ 215  
 233 VALPVQSPASAGPANNPLNLFPGGVPS-----GSPGVVPPAGSQA 275

216 FARMDPN-AGMGASGAGASAPP--APGGDAPEEGSNTNTSSNTGNAGTNA 272  
 276 LDALROLPOFQALQLVQANP--QLIQPMLOELGKONPOLRLIOENQAEFLRLNESPE 333  
 273 NFA-----ANPFAASLNPL-----NP-----FANAGNRAST 299  
 334 GGGGNN--ILGOLAAVPOTL---TVPEER-EAIOELEMGF 370  
 300 GMPAFDPALLASMFQPPVQASQAEPTRPPEEREYHQLRLNDMGF 344  
 RESULT 8  
 YADG\_SCHPO STANDARD; PRI: 354 AA.  
 ID YADG\_SCHPO  
 AC Q10169;  
 DT 01-OCT-1996 (rel. 34, created)  
 DT 01-OCT-1996 (rel. 34, last sequence update)  
 DT 15-JUN-2002 (rel. 41, last annotation update)  
 DE Hypothetical protein C26A3.16 in chromosome I.  
 GN SPAC26A3.16.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 DR MEDLINE=21848401; PubMed=11859360;  
 DR Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Monep P., Moule S., Mungall K., Murphy L., Nidlett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,  
 RA Wellens I., Vansireels E., Rieger M., Schefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,  
 RA Shpakovskii G.V., Ussery D., Barrell B.G., Nurse P.;  
 RA "The genome sequence of Schizosaccharomyces pombe.";  
 RT Nature 415:871-880(2002).  
 RL Nature 415:871-880(2002).  
 CC -1- SIMILARITY: TO YEAST DSK2.  
 CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.  
 -----  
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 CC EMBL: Z69240; CA93239.1;  
 DR InterPro: IPR000449; UBA\_domain.  
 DR InterPro: IPR000526; Ubiquitin.  
 DR Pfam: PF00240; ubiquitin.1.  
 DR Pfam: PF00627; UBA.1.  
 DR SMART: SM00165; UBA.1.  
 DR SMART: SM00213; UBO.1.





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Db 214 SLVNNGBA-----ALPLPKPAAPGVITQTPFVGAAPADPAASPPAPAPAPAAA 267
Qy 113 PTOAPVATETAPPVQPOQAPAPATVAATDDADVYSQAASNLVFNLEQTIOOIIDMG 172
Db 268 PPPPPAPATLAPRPGHAPGPPTAAPAVPPPA-----AQN-----G 304
Qy 173 GTWERPTVVRAALRAAYNNEPRAIDVYSGIPEVNEAP-----VARAPAAQOQTNQ----- 223
Db 305 GS-----AGAAPAPAPPA-----AGGPAGVSGCPGGAAGAAAPAPGVKAESPRTVY 349
Qy 224 QAASPAQAPVALVPPSPASPA-----GPNANPLNFPQGV--PSCGSNPGVVPAGSGALDA 278
Db 350 QAAPPAAGTILASGSPASTASWITGPTMGALFSPAAPVPPAPGTPGLPKGAAGAVTOS 409
Qy 279 LRQLPQ-----FQALLQVQANPQIQLPMLDELKONPOI---LRLIQENAEFLRYNE 330
Db 410 LSTPTATISGIRATLTPYTLARLPQPPQNPINIQNFQLPQGMVLVRSNGULMIPOQ 469
Qy 331 SPEGPGCNILGOLAA---AVPQTLTVTP 356
Db 470 A-----LAOMQAQAHAPQOT-TMAP 488

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RESULT 10
ODP2_AZOV1
ID ODP2_AZOV1 STANDARD; PRT; 637 AA.
AC P10802;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2).
OS Azobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 478;
RX MEDLINE=88271330; PubMed=3292237;
RA Hanemaaijer R., Janssen A., de Kok A., Veeger C.;
RT "the dihydrolipoalyltransferase component of the pyruvate
RT dehydrogenase complex from Azobacter vinelandii. Molecular cloning
RT and sequence analysis."
RL Eur. J. Biochem. 174:593-599(1988).
RN [2]
RP SEQUENCE OF 1-15 AND 380-415.
RX MEDLINE=88082750; PubMed=3691494;
RA Hanemaaijer R., de Kok A., Jolles J., Veeger C.;
RT "The domain structure of the dihydrolipoalyl transferase component
RT of the pyruvate dehydrogenase complex from Azobacter vinelandii."
RL Eur. J. Biochem. 169:245-252(1987).
RN [3]
RP LIPOYL DOMAIN CONFORMATION.
RX MEDLINE=89052887; PubMed=3191993;
RA Hanemaaijer R., Vervoort J., Westphal A.H., de Kok A., Veeger C.;
RT "Mobile sequences in the pyruvate dehydrogenase complex, the E2
RT component, the catalytic domain and the 2-oxoglutarate dehydrogenase
RT complex of Azotobacter vinelandii, as detected by 600 MHz 1H-NMR
RT spectroscopy."
RL FEBS Lett. 240:205-210(1988).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 381-637.
RX MEDLINE=92196586; PubMed=1549782;
RA Matevli A., Obojlova G., Schulze E., Kalk K.H., Westphal A.H.,
RA de Kok A., Hol W.G.J.;
RT "Atomic structure of the cubic core of the pyruvate dehydrogenase
RT multienzyme complex."
RL Science 255:1544-1550(1992).
RN [5]
RP STRUCTURE BY NMR OF 1-78.
RX MEDLINE=94422112; PubMed=8068086;

```

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RA Berg A., de Kok A., Vervoort J.;
RT "Sequential 1H and 15N nuclear magnetic resonance assignments and
RT secondary structure of the N-terminal lipoyl domain of the
RT dihydrolipoalyl transferase component of the pyruvate dehydrogenase
RT complex from Azotobacter vinelandii."
RL Eur. J. Biochem. 221:87-100(1994).
RN [6]
RP STRUCTURE BY NMR OF 1-78.
RX MEDLINE=97234563; PubMed=9119000;
RA Berg A., Vervoort J., de Kok A.;
RT "Three-dimensional structure in solution of the N-terminal lipoyl
RT domain of the pyruvate dehydrogenase complex from Azotobacter
RT vinelandii."
RL Eur. J. Biochem. 244:352-360(1997).
CC -1- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
CC acetyldihydrolipoamide.
CC -1- COFACTOR: THE E2 COMPONENT CONTAINS THREE COVALENTLY-BOUND LIPOYL
CC COFACTORS.
CC -1- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH OCTAHEDRAL
CC SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -1- SIMILARITY: CONTAINS 3 LIPOYL-BINDING DOMAINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X12455; CAA30987.1; ALT_INIT.
DR PIR: S01017; XXAV.
DR PDB: 1EAA; 31-OCT-93.
DR PDB: 1EAB; 31-OCT-93.
DR PDB: 1EAC; 31-OCT-93.
DR PDB: 1EAD; 31-OCT-93.
DR PDB: 1EAE; 31-OCT-93.
DR PDB: 1EAF; 31-OCT-93.
DR PDB: 1IYU; 12-MAR-97.
DR PDB: 1IYV; 12-MAR-97.
DR PDB: 1DPB; 20-APR-95.
DR PDB: 1DPC; 20-APR-95.
DR PDB: 1DPD; 20-APR-95.
DR InterPro: IPR001078; 2Oxoacid_dh.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR004167; E3_binding.
DR InterPro: IPR003016; Lipoyl.
DR Pfam: PF00198; 2-oxoacid_dh; 1.
DR Pfam: PF0364; biotin_lipoyl; 3.
DR Pfam: PF02817; e3_binding; 1.
DR PRODOM: PD001115; 2Oxoacid_dh; 1.
DR PROSITE: PS00189; LIPOYL; 3.
KW Glycolysis; Transferase; Acyltransferase; Repeat; Lipoyl;
KW 3D-structure.
FT INTI_MET 0
FT DOMAIN 1 326 0
FT DOMAIN 327 380 LIPOYL BINDING.
FT DOMAIN 381 637 E1/E3 BINDING.
FT BINDING 39 39 CATALYTIC.
FT BINDING 156 156 LIPOYL (POTENTIAL).
FT BINDING 261 261 LIPOYL (POTENTIAL).
FT REPEAT 1 115 LIPOYL (POTENTIAL).
FT REPEAT 116 220 LIPOYL (POTENTIAL).
FT REPEAT 221 326 LIPOYL (POTENTIAL).
FT ACT_SITE 610 610
FT HELIX 403 406
FT HELIX 416 431
FT POTENTIAL.

```



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FT STRAND 434 442
FT HELIX 444 452
FT TURN 453 453
FT HELIX 454 459
FT TURN 460 461
FT HELIX 466 480
FT HELIX 482 484
FT STRAND 486 488
FT TURN 490 491
FT STRAND 495 497
FT STRAND 503 505
FT STRAND 507 509
FT TURN 510 511
FT STRAND 512 514
FT STRAND 517 518
FT HELIX 521 523
FT HELIX 526 541
FT TURN 542 543
FT HELIX 547 550
FT STRAND 555 559
FT TURN 561 563
FT TURN 574 575
FT STRAND 578 582
FT STRAND 586 591
FT STRAND 596 609
FT TURN 612 612
FT HELIX 615 630
FT HELIX 632 636
SQ SEQUENCE 637 AA; 64913 MW; D0603BA4A385F84 CRC64;
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Query Match 7.1%; Score 144; DB 1; Length 637;  
Best Local Similarity 22.5%; Pred. No. 0.28;  
Matches 80; Conservative 39; Mismatches 149; Indels 88; Gaps 11;

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QY 19 PDASVADVKKIIT-NOGSTYRADQOMLYOGKILKDETTLESGVYENSFLYIMLSKA 77
DB 122 PDGSGAKAVIEVLKAGVOQAEGLVLESKASMEIIPSPASGVES--VAIQUNAE 179
QY 78 KASSSGASTATKAPATLLOPAAPVAPASVATPTQAPVATAPETAPPSVO---PQAA 133
DB 180 VGTGDLILFLRTTGA-----QAOPFAPAAAAASPAPAPLAPAAAGPOEVKVDIGSAG 233
QY 134 PAATVATDDADYVSOASLVFGNNLEORTIQOILDMGGTWERDITVYRLRAYNNPER 193
DB 234 KAVIEVLKAGDOVQAEQSLI-----VLESDKASMEIIPSP 269
QY 194 AIDYISGIPENYEAOPVARAPAPAGQOTNOQASPAQPAVALPYQSPASAGPANPLNL 253
DB 270 A-----AGVESVAVOLNAEVTGDDILITRVAGAAPSGFRAGSPFOQAAAAPAPAPA 324
QY 254 FPGVPSGSGNPVPGAGGALDALRQLPQFALLQVQANPQILOPMLQELCKQNPQI 313
DB 325 -PYGAPSRN-----GAKVHAGPAVRQL-----AREGVE----- 352
QY 314 LRLIQEQAQAEFLKLVNESPBGEGNLTGOLAAAVPOTLVTPPERAIOQLBSMG 369
DB 353 -----LAINST---GPRGRLKEDVQAYVYVAMQKAEAPAGASAG 394

RESULT 11
GSRL_HUMAN STANDARD; PRT; 1509 AA.
AC 09NM24;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glioma tumor suppressor candidate region gene 1 protein.
GN GLTSCR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE-20175430; PubMed-10708517;
RA Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
RA Portier B.P., Ueki K., Billings S., Ramaswamy S., Mohrenweiser H.W.,
RA Scheithauer B.W., Louis D.N., Jenkins R.B.;
RT "A transcript map of the chromosome 19q-Arm glioma tumor suppressor
RT region." 64:44-50(2000).
RL Genomics 64:44-50(2000).
CC -1- TISSUE SPECIFICITY: Expressed at moderate levels in heart, brain,
CC placenta, skeletal muscle, and pancreas, and at lower levels in
CC lung, liver, and kidney.
CC -----
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Query Match 6.9%; Score 140.5; DB 1; Length 1509;  
Best Local Similarity 23.5%; Pred. No. 1.2;  
Matches 108; Conservative 36; Mismatches 135; Indels 181; Gaps 24;

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QY 55 DETLESNGVA-ENSPFIVM--ISKAKASS-----SGASATNT-----AAPA 94
DB 220 EPTVLASAGVSPGAGATVQKNTLSAAVATLTNGSVFEGAGAAAPGTSPGQPLAIVPG 279
QY 95 TLAQAPAVAPASVATPTQAPVATAPETAPPSV-----OQAPAPATVATDDADYVSO 149
DB 280 LGSSPLVP-APNVILHRTPTIPQPKVAGVLPKLYQLPKFAPAGATITVIGSRPALPQ 338
QY 150 ---AASLVFGNNLEQTTIQOILDMGGTWERDITVR---ALR-----AAY 188
DB 339 QPKAPQNLTF-----MAAGKAGQNVLSGFPAAPALQANVFKQPPATTTGAAP 385
QY 189 NNPERAT-----DYLXSG-----IPENYEAQ----- 210
DB 386 PDPGALSKRPSVHLNQGSSIVTPAQHMLPGQNOFILPGAPAVQLPQQLSALPANYGQ 445
QY 211 --VARAPAGQO-----TNOQASP-----AQPAV-- 233
DB 446 ILAAPHHTGGQLANPLITNQNLAGPLSLGPLYAPHSAGASAILLSAAPIQVQAPLFPQ 505
QY 234 -----ALPVPSPASAGPNANP-----INLFPQV-----PSGGSNPGVVPAGSGAL 276
DB 506 MPVSLAAGSLPTQSPAPAGPAATTVLQGVTLPPSAVAMLNTPGVLQVAPATPAATGEAA 565
QY 277 DALRQLPQFALLQVQANPQILOPMLQELCKQNPQILRLIQEQAQAEFLRLV-----NESP 332
DB 566 PVLTVQ-----APQAPVAVSTPL--PLGLQDPQAO---QPPQAPTPOAAAPQOATTP 613
QY 333 EGGPG-----GNILGOLAAAVPOTLVN-----TPPER 359
DB 614 QPSPGLASSPEKTVLGQPPSATPTAIIITQDSLOMFLPQER 653

RESULT 12
CBP_MOUSE STANDARD; PRT; 2441 AA.
ID CBP_MOUSE
AC P45481;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
```

DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE CREB-binding protein.  
 GN CREBBP OR CBP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA MEDLINE=94019866; PubMed=8413673;  
 RA Christia J.C., Kwok R.P.S., Lamb N., Haglware M., Montminy M.R.,  
 RA Goodman R.H.;  
 RL "Phosphorylated CREB binds specifically to the nuclear protein CBP.",  
 Nature 365:855-859(1993).  
 CC -1- FUNCTION: MEDIATES CAMP-GENE REGULATION BY BINDING SPECIFICALLY TO  
 PHOSPHORYLATED CREB PROTEIN. ACTING AS A COACTIVATOR, CBP ARGUMENTS  
 THE ACTIVITY OF PHOSPHORYLATED CREB TO ACTIVATE TRANSCRIPTION OF  
 CAMP-RESPONSIVE GENES.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: CONTAINS 1 BROMODOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 Z2-TYPE ZINC FINGER.  
 CC -----  
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 CC -----  
 DR EMBL: S66385; AAB28651.1; -  
 DR TRANSFAC: T01318; -  
 DR MGD: MGI:1098280; Crebbp.  
 DR InterPro: IPR001487; Bromodomain.  
 DR InterPro: IPR003101; KIX.  
 DR InterPro: IPR000197; TAZ\_finger.  
 DR InterPro: IPR000433; ZnF\_ZZ.  
 DR Pfam: PF00439; bromodomain.1.  
 DR Pfam: PF00569; ZZ.1.  
 DR Pfam: PF02135; ZF\_TAZ.2.  
 DR Pfam: PF02172; KIX.1.  
 DR PRINTS: PRO0503; BROMODOMAIN.  
 DR SMART: SM00297; BROMO.1.  
 DR SMART: SM00291; ZnF\_ZZ.1.  
 DR PROSITE: PS00633; BROMODOMAIN\_1; 1.  
 DR PROSITE: PS01357; BROMODOMAIN\_2; 1.  
 DR PROSITE: PS01357; ZF\_ZZ.1; 1.  
 DR PROSITE: PS01357; ZF\_ZZ.2; 1.  
 KW Transcription regulation; Nuclear protein; Activator; Bromodomain;  
 KW Zinc-finger.  
 FT DOMAIN 1104 1176 BROMODOMAIN.  
 FT ZN\_FING 1702 1745 Z2-TYPE.  
 FT DOMAIN 1062 1065 POLY-GLU.  
 FT DOMAIN 1556 1563 POLY-GLU.  
 FT DOMAIN 1944 1949 POLY-PRO.  
 FT DOMAIN 1968 1971 POLY-GLN.  
 FT DOMAIN 2082 2086 POLY-GLN.  
 FT DOMAIN 2200 2216 POLY-GLN.  
 FT DOMAIN 2296 2299 POLY-GLN.  
 SQ SEQUENCE 2441 AA; 265474 MW; 0AB8028C3112F419 CRC64;  
 Query Match 6.9%; Score 140; DB 1; Length 2441;  
 Best Local Similarity 21.7%; Pred. No. 2.1;  
 Matches 92; Conservative 41; Mismatches 159; Indels 132; Gaps 18;  
 QY 44 QMLTYGKILDE-TTLESNGVAENSFLVIMLSKAKSSGASTATTAATLQAQPAAP 102  
 DB 1857 QHCQQAQMLARRAATMTATRVPOSL-----PSPISAPETPTQOSTPOTPOPP 1907  
 QY 103 VAPAS-----VART--PT---QAPVATETAPPSPVQQAAPAAVATADAD 145  
 DB 1908 AQPSPVNNSPAGFPVNAVPTQPTIVSAGKPTNOVPAPPPAPD---PRAVEAARQIE 1964

QY 146 VYQAASNLVFGNNLEQTTIQIILDMGGGTWERDVTYVRLRAAYNNPERAIDYLSGIEP- 204  
 DB 1965 REAQOQOQHLYRAN-----INNGMPG-----RDMGRTPGSGMTVGLNVRPP 2006  
 QY 205 NVEADQVNAAPAAAGQOTN---QQAASPAQPAVALPVQPSPASAGBNANPLNFPQGVPS 260  
 DB 2007 NOVSGFVNSMPPGGWQQAIPQOQPMPCMPPRVSMQAQAAVAGPR-----MPN 2056  
 QY 261 GGSNPGVVGAGSGALDALROL-----PQFALLQLYVANPQIL----- 299  
 DB 2057 VQPNNSISP---SALQDLRLTKSPSSPQOQOQVILNLSNPQLMAAFIKQRTANYANQ 2113  
 QY 300 -----QPMLOELGKONPQ-----ILRLIQNQAQFLRLVNESPEGGPG-NILGQLAA 346  
 DB 2114 PCMQPQGLQSPGCMQPGCMHQPSLQVLMQAGVPRPGVPPQPMGSLNPGQALN 2173  
 QY 347 AV-----PQTLVTPEERAIQRLBGMCFNRLVLEVFACKNDELRYANVLDHGHEPD 401  
 DB 2174 INNPGHNPMPTMNPQYREVR-----QLLQHQOQOQ 2206  
 QY 402 DQOQ 405  
 DB 2207 QOQO 2210  
 RESULT 13  
 BAT3\_HUMAN STANDARD; PRT; 1132 AA.  
 ID BAT3\_HUMAN  
 AC P46379;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Large proline-rich protein BAT3 (HLA-B-associated transcript 3).  
 GN BAT3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RA MEDLINE=90192810; PubMed=2156268;  
 RA Banerji J., Sands J., Strominger J.L., Spies T.;  
 RT "A gene pair from the human major histocompatibility complex encodes  
 large proline-rich proteins with multiple repeated motifs and a  
 single ubiquitin-like domain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2374-2378(1990).  
 CC -1- FUNCTION: UNKNOWN.  
 CC -1- SIMILARITY: CONTAINS 1 UBIQUITIN-LIKE DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: M33519; AAA35587.1; -  
 DR EMBL: M33521; AAA35588.1; -  
 DR EMBL: M33520; AAA35588.1; JOINED.  
 DR HSSP: P02248; IOBI.  
 DR Genew: HGNC:13919; BAT3.  
 DR MIM: 142590; -  
 DR InterPro: IPR000626; Ubiquitin.  
 DR Pfam: PF00240; ubiquitin.1.  
 DR SMART: SM00213; UBQ.1.  
 DR PROSITE: PS00299; UBIQUITIN\_1; 1.  
 DR PROSITE: PS00553; UBIQUITIN\_2; 1.  
 KW Repeat.  
 FT DOMAIN 17 77 UBIQUITIN-LIKE.  
 FT DOMAIN 202 207 POLY-PRO.



